That which is claimed is:

1. A method of discriminating among a plurality of nucleic acid targets, the method comprising:

identifying differences in the extent of nucleic acid duplex formation between each of said nucleic acid targets and at least one common nucleic acid probe, wherein each of said duplexes is formed in a hybridization reaction in the presence of a specific association enhancer under conditions suitable for association of duplexes.

2. The method of claim 1, wherein said specific association enhancer is a cationic detergent.

3. The method of claim 2, wherein said cationic detergent is selected from the group consisting of tetradecyltrimethylammonium salts, cetyltrimethylammonium salts, and octadecyltrimethylammonium salts.

4. The method of claim 3, wherein said cationic detergent is selected from the group consisting of cetyltrimethylammonium bromide (CTAB), cetyltrimethylammonium chloride (CTAC), cetyltrimethylammonium hydrosulfate (CTAS), tetradecyltrimethylammonium bromide (TTAB), and octadecyltrimethylammonium bromide (OTAB).

5. The method of claim 4, wherein said cationic detergent is cetyltrimethylammonium bromide.

6. The method of claim 1, wherein each of said duplexes includes a molecule of RNA and a molecule of DNA.

7. The method of claim 1, wherein said each of said duplexes includes two molecules of RNA.

8. The method of claim 1, wherein each of said duplexes includes a molecule of DNA molecule and a molecule of modified DNA (mDNA).

9. The method of claim 8, wherein the mDNA molecule includes at least one nucleotide modified at the 2' carbon of ribose.

10. The method of claim 1, wherein said at least one common probe comprises a region of complementarity to at least one of said targets at least 16 nucleotides in length.

11. The method of claim 1, wherein said at least one common probe comprises a region of complementarity to at least one of said targets no more than 30 nucleotides in length.

12. The method of claim 1, wherein each of said duplexes includes a nucleic acid molecule no more than 30 nt in length.

13. The method of claim 12, wherein each of said duplexes includes a nucleic acid molecule at least 16 nt in length.

14. The method of claim 13, wherein each of said duplexes includes a nucleic acid molecule 16 - 30 nt in length.

15. The method of claim 1, wherein said plurality of targets includes at least 5 targets of distinct sequence.

16. The method of claim 15, wherein said plurality of targets includes at least 100 targets of distinct sequence.

17. The method of claim 1, wherein said targets are genomic DNA.

18. The method of claim 1, wherein said targets are mRNA or cDNA.

19. The method of claim 1, wherein said targets are derived from mammalian nucleic acids.

20. The method of claim 19, wherein said mammalian nucleic acids are human nucleic acids.

21. The method of claim 1, wherein said at least one common probe is genomic DNA.

22. The method of claim 1, wherein said at least one common probe is mRNA or cDNA.

23. The method of claim 1, wherein said common probe is derived from mammalian nucleic acids.

24. The method of claim 23, wherein said mammalian nucleic acids are human nucleic acids.

25. The method of claim 1, wherein said duplexes are formed in a common hybridization reaction.

26. The method of claim 1, wherein said hybridization reactions are single phase solution reactions.

27. The method of claim 1, wherein said common probe, or each of said targets, is immobilized on a substrate.

28. The method of claim 1, wherein said probe, or each of said targets, is detectably labeled.

29. The method of claim 1, wherein said hybridization reactions comprise less than about 0.7M salt.

30. The method of claim 1, wherein said hybridization reactions are performed at a temperature of no more than about 60°C.

31. The method of claim 1, wherein at least two of said plurality of targets differ in sequence by no more than a single nucleotide.

32. The method of claim 1, further comprising, after duplex formation:
adding salt to hybridization reaction; and
removing or diluting said specific association enhancer.

33. The method of claim 1 or claim 32, further comprising:
separating said nucleic acid duplexes from said hybridization reactions for use in a subsequent enzymatic reaction.

34. A method of performing a hybridization-primed enzymatic reaction, comprising:
hybridizing at least one nucleic acid primer to a nucleic acid template in the presence of an effective amount of a specific association enhancer, wherein said at least one primer has a region of complementarity to said template, and then
performing an enzymatic reaction on said duplexed primer.

35. The method of claim 34, wherein said primer is DNA and said template is RNA.

36. The method of claim 34, wherein said primer is RNA and said template is DNA.

37. The method of claim 34, wherein said specific association enhancer is a cationic detergent.

38. The method of claim 37, wherein said cationic detergent is selected from the group consisting of tetradecyltrimethylammonium salts, cetyltrimethylammonium salts, and octadecyltrimethylammonium salts.

39. The method of claim 38, wherein said cationic detergent is selected from the group consisting of cetyltrimethylammonium bromide (CTAB), cetyltrimethylammonium chloride (CTAC), cetyltrimethylammonium hydrosulfate (CTAS), tetradecyltrimethylammonium bromide (TTAB), and octadecyltrimethylammonium bromide (OTAB).

40. The method of claim 39, wherein said cationic detergent is cetyltrimethylammonium bromide.

41. The method of claim 34, wherein said enzymatic reaction is selected from the group consisting of: polymerization, nuclease digestion, phosphatasing, phosphorylation, methylation, and ligation.

42. The method of claim 41, wherein said enzymatic reaction is polymerization.

43. The method of claim 34, further comprising the step, after probe hybridization and before enzymatic reaction, of:

removing said specific association enhancer.

44. The method of claim 43, further comprising the step, before removing said specific association enhancer, of :

adding salt to said hybridization reaction.

45. A method for increasing the specific association rate of a pair of single-stranded nucleic acid molecules, the method comprising:

combining in a reaction mixture a first single-stranded molecule and a second single-stranded molecule in the presence of an association enhancer, said combining being under conditions suitable for specific association of the first and second molecules in a nucleic acid duplex,

wherein said combining allows for formation of matched nucleic acid duplexes at an increased specific association rate.